

Sub A17
SEQUENCE SUBMISSION

SEQ ID NO: 1 is a mouse 312C2 nucleic acid sequence.
SEQ ID NO: 2 is a mouse 312C2 amino acid sequence.
SEQ ID NO: 3 is a human 312C2 nucleic acid sequence.
SEQ ID NO: 4 is a human 312C2 amino acid sequence.
SEQ ID NO: 5 is a reverse translation sequence.
SEQ ID NO: 6 is clone A8 amino acid sequence.
SEQ ID NO: 7 is clone A5 amino acid sequence.
SEQ ID NO: 8 is clone G10 amino acid sequence.

SEQUENCE LISTING

15 (1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert

20 (ii) TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
Reagents

25 (iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
30 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

35 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

40 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Not yet assigned
(B) FILING DATE: August 14, 1997
(C) CLASSIFICATION:

45 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,419
(B) FILING DATE: 16-AUG-1996

50 (viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/027,901
(B) FILING DATE: 07-OCT-1996

55 (ix) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0612K1

60 (x) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE:
(B) TELEFAX:

(2) INFORMATION FOR SEQ ID NO:1:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 68..754
(D) OTHER INFORMATION:

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25 CTCGAGATCC ATTGTGCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG 60
AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT 109
Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
1 5 10
GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC 157
Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
15 20 25 30
30 CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC 205
Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
35 40 45
35 CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT 253
Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
50 55 60
40 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG 301
Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
65 70 75
45 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT 349
His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
80 85 90
50 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA 397
Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
95 100 105 110
55 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA 445
Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
115 120 125
55 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC 493
Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
130 135 140
60 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC 541
Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe

	145	150	155	
	CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC			589
5	Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly			
	160	165	170	
	CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC			637
	Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr			
10	175	180	185	190
	CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC			685
	Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe			
	195	200	205	
15	CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT			733
	Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His			
	210	215	220	
20	CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAACGC			781
	Leu Gly Gly Arg Trp Pro			
	225			
	CAGACGCTAC AAGACTTGCC CAGCTATAACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC			841
	CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG			901
25	TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTGGA CAGCTCTGTT GGAGTAGGGT			961
	CTTTGGGCC ACCAAGAGCA CCACGTTAG CACAAGATCT TGTACAAGAA TAAATACTTG			1021
30	TTTAGTAACC TGAAAAAAA AAAAAGG GCGGCCGCGG AGGCCGAATT CC			1073

(2) INFORMATION FOR SEQ ID NO:2:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Ala	Trp	Ala	Met	Leu	Tyr	Gly	Val	Ser	Met	Leu	Cys	Val	Leu	
1					5					10					15	
45	Asp	Leu	Gly	Gln	Pro	Ser	Val	Val	Glu	Glu	Pro	Gly	Cys	Gly	Pro	Gly
							20		25						30	
50	Lys	Val	Gln	Asn	Gly	Ser	Gly	Asn	Asn	Thr	Arg	Cys	Cys	Ser	Leu	Tyr
								35		40					45	
55	Ala	Pro	Gly	Lys	Glu	Asp	Cys	Pro	Lys	Glu	Arg	Cys	Ile	Cys	Val	Thr
							50		55						60	
65	Pro	Glu	Tyr	His	Cys	Gly	Asp	Pro	Gln	Cys	Lys	Ile	Cys	Lys	His	Tyr
							65		70						80	
80	Pro	Cys	Gln	Pro	Gly	Gln	Arg	Val	Glu	Ser	Gln	Gly	Asp	Ile	Val	Phe
							85			90					95	

Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
 100 105 110

5 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
 115 120 125

Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
 130 135 140

10 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
 145 150 155 160

Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
 165 170 175

15 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
 180 185 190

20 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
 195 200 205

Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
 210 215 220

25 Gly Arg Trp Pro
 225

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1006 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..723

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
 ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG
 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
 1 5 10 15

50 GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC
 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
 20 25 30

55 GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC
 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
 35 40 45

60 TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG
 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
 50 55 60

48

96

144

192

	GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 65 70 75 80	240
5	TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 85 90 95	288
10	GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 100 105 110	336
15	ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 115 120 125	384
20	AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 130 135 140	432
25	GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 145 150 155 160	480
30	GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 165 170 175	528
35	GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 180 185 190	576
40	AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val 195 200 205	624
45	CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 210 215 220	672
50	CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 225 230 235 240	720
55	GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGGCCAGC CCCTCCCCAG Val	773
60	GAGCTCCCCA, GGCCGCAGGG GCTCTGCCTT CTGCTCTGGG CGGGGCCCTG CTCCCCCTGGC AGCAGAAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTCGGCGG CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT GTCACCTAAA TTCAATTACAC TGGCCGTGCGT TTTACAACGT CCTGACTGGG AAA	833 893 953 1006

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110

Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125

Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
165 170 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
180 185 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
195 200 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
210 215 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
225 230 235 240

55 Val

(2) INFORMATION FOR SEQ ID NO:5:

60

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNNGCNYTNT GYGGNYTNNGC NYTNYTNTGY
GCNYTNWSNY TNGGNCARMG NCCNACNGGN GGNCCNGGNT GYGGNCCNGG NMGNYTNYTN
YTNGGNACNG GNACNGAYGC NMGNNTGYTGY MGNGTNCAYA CNACNMGNTG YTGYMGNGAY
20 TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY
TGYYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN
CARWSNCARG GNAARTTYWS NTYYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY
25 WSNGGGNGNC AYGARGGNCA YTGYAARCCN TGGACNGAYT GYACNCARTT YGGNTTYYTN
ACNGTNTTYC CNGGNAAYAA RACNCAYAAY GCNGTNTGYG TNCCNGGNWS NCCNCCNGCN
30 GARCCNYTNG GNTGGYTNAC NGTNGTNYTN YTNGCNGTNG CNGCNTGYGT NYTNYTNYTN
ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGNW SNCARTGYAT GTGGCCNMGN
35 GARACNCARY TNYTNYTNGA RGTNCCNCCN WSNACNGARG AYGCNMGNWS NTGYCARTTY
CCNGARGARG ARMGNGGNGA RMGNWSNGCN GARGARAARG GNMGNYTNNG NGAYYTNTGG
720

40 (3) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

60

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

5 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110

15 Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125

20 Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160

25 Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Lys Thr Gln Leu Leu
180 185 190

30 Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro
195 200 205

35 Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly
210 215 220

Asp Leu Trp Val
225

40 (2) INFORMATION FOR SEQ ID NO:7:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

60

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

5 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Ser Trp Arg Cys Leu Trp Glu Ser Thr Gln Ala Arg Gly
100 105 110

15 Ser Thr Arg Ala Arg Gly Arg Ala Arg Gly His Arg Cys Pro Ala Arg
115 120 125

20 Thr Cys Gly Val Trp Gly Pro Glu Ser Cys Glu Ala Gly Gln Ala Arg
130 135 140

Pro Cys Ser Gly Thr Thr Gly His Glu Ala Leu Gly Val Ser Cys Pro
145 150 155 160

25 Cys Phe Leu Ser Leu Gly Phe Ser Ile Gln His Glu Gly Cys Glu Asn
165 170 175

30 Pro Ala Gly Arg Trp Gly Arg Val Pro Gly Ala Val Trp Leu Ser Gly
180 185 190

Pro Gly His Pro Ser Cys Leu Ser Ser Pro His Thr Glu Arg Ala Cys
195 200 205

35 Pro Val Pro Pro Gly Val Leu Ser Gly Ala Trp Gly Cys Thr Leu Phe
210 215 220

Trp Lys Glu Gln Leu Lys Ser Ser
225 230

40 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids
45 (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
60 20 25 30

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

5 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

10 Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110

15 Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125

20 Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160

25 Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp
180 185 190

30 Pro Arg Gly Leu Ser Gln Pro Gly Ala Gly Arg Trp Glu His Gly Cys
195 200 205

35 Leu Leu Thr Val Ala Pro Leu Gln Arg Pro Ser Cys Cys Trp Arg Cys
210 215 220

Arg Arg Arg Pro Lys Thr Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser
225 230 235 240

40 Gly Ala Ser Asp Arg Gln Arg Arg Gly Gly Trp Glu Thr Cys Gly
245 250 255

Cys Glu Pro Gly Arg Pro Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser
260 265 270

45 Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg
275 280 285

50 Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp
290 295 300

Gln Arg Pro Gly Pro Cys Ser
305 310

55